

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 142282

TO: James Schultz

Location: REM-2D18 \$2C18

Art Unit: 1635

Tuesday, January 25, 2005

Case Serial Number: 09163289

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Schultz,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



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142232

From: Sent:

Schultz, James

To:

Tuesday, January 11, 2005 11:24 AM

Subject:

STIC-Biotech/ChemLib Sequence search 09/163,289

Hello,

I need a standard nucleotide sequence search run against SEQ ID NO:3 in the above entitled application. Please include the interference databases.

Thanks, Doug Schultz

James Douglas Schultz, PhD AU 1635 (Biotechnology) Patent Examiner United States Patent and Trademark Office (Office) REM 2D18 (Mail) REM 2C18 (571) 272-0763 RE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2Date Searcher Picked up: ____
Date Completed: ____
Searcher Prep/Rev. Time: ____
Online Time: ____

Type of Search

NA Sequence: #_____

AA Sequence :#____

Structure: #____

Bibliographic:_____

Litigation:____

Patent Family:_____

Other:____

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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Listing first 45 summaries
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REFERENCE AUTHORS TITLE JOURNAL DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AR091456 LOCUS 밁 á 밁 á 밁 5 밁 Ş ORIGIN FEATURES Query Match 76.2 Best Local Similarity 69.6 Matches 149; Conservative source 178 122 61 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAAUGUGGGAAACUCGACU 120 62 ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCCAAATGTGGGAAACTCGACT 1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU li (bases 1 to 215) Dietz,H.C. Mammalian regulator of nonsense-mediated Patent: US 5994119-A 26 30-NOV-1999; Location/Qualifiers AR091456 215 bp Sequence 26 from patent US 5994119. AR091456 N Unclassified. Unknown AR091456.1 Unknown. AUCUAGUGGGGACUGCGUUCGCGCUUUCCCCUG 211 GCTAGTGGGGACTGCGTTCGCGCTTTCCCCTG GCAGAATTGTTGTAGCACTCCAGCTGATGAGTCCGTGAGGACGAAACTGTCTCCCCCAGG 181 ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCCAGGGCGAGGCTT /organism="unknown" /mol_type="unassigned DNA" .215 GI:10018211 76.2%; Score 160.8; DB 6; 69.6%; Pred. No. 1.1e-40; cive 45; Mismatches 17; DNA RNA Indels Length 215; linear PAT 07-SEP-2000 ω •• Gaps 177 121 61 60

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                                                                                                                                                     artificial sequences.

1 (Dases 1 to 164)

Murakami,A. and Kojima,K.

Methods and kits for measuring antibodies against ENA

Patent: WO 0190756-A 3 29-NOV-2001;

MEDICAL & BIOLOGICAL LABORATORIES CO LTD,AKIHIRO MURAKAMI,
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Agris, P.F., KiKuChi,Y., Gross,H.J., Takano,M. and Sharp,G.C. Characterization of the autoimmune antigenic determinant for ribonucleoprotein (RNP) antibody
Immunol. Commun. 13 (2), 137-149 (1984)
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                                                                     Artificial Sequence
WO 0190756-A/3
29-NOV-2001
21-MAY-2001 WO 2001JP004251
26-MAY-2000 JP 00P 157410
AKIHIRO MURAKAMI, KAZUO KOJIMA
                                              Description of Artificial Sequence: Artificially synthesized
                                                            G01N33/564
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             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/mol_type="snRNA"
/db_xref="taxon:9913"
/tissue_type="thymus"
/dev_stage="calf"
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    /organism='Artificial Sequence'.

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Pred. No. 5.8e-30;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 165)

Branlant, C., Krol, A., Ebel, J.P., Lazar, E., Gallinaro, H., Jacob, M.,

Sri-Widada, J. and Jeanteur, P.

Nucleotide sequences of nuclear UlA RNAs from chicken, rat and man

Nucleic Acids Res. 8 (18), 4143-4154 (1980)
                                                                                                                                                                                                                                                                                                                     Mg2+ induces a sharp and reversible transition nuclear ribonucleoprotein configurations Mol. Cell. Biol. 4 (9), 1890-1899 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. I
85134903
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                                                                                                                                                                                                                               Original source text: Human HeLa cell uRNA.
The trimethylguanosine cap was experimentally
Location/Qualifiers
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Lin, W.L. and Pederson, T.
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K00788.1 GI:174936
U1 small nuclear RNA.
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                                                                                                                                                         /organism="Homo sapiens"
/mol_type="snRNA"
/db_xref="taxon:9606"
/gene="RNU1"
/note="trimethylguanosine cap [1],[2]"
                                                        /gene="RNU1"
/note="U1 small
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                            Unclassified.

1 (bases 1 to 203)

1 (bases 1 to 203)

Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.

EST's and encoded human proteins

Patent: US 6639063-A 16454 28-OCT-2003;

Location/Qualifiers
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                                                                                                                         l Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                    Sequence 16454 from patent AR424957 AR424957.1 GI:40180067
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GCAGAAUUGGCGAU 134
                                        AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUUCCCCAAAUGUGGGAAAACUCGACU 120
                                                                       ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
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                                                                                                                       60.5%; Score 127.6; DB 6 llarity 73.1%; Pred. No. 5.8e-30; Conservative 32; Mismatches 4
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/mod_base=OTHER
of UIA uRNA.
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/mol_type="genomic DNA"
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/mod_base=OTHER
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/mod_base=OTHER
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/note="pseudouridine
/mod_base=OTHER
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|mod_base=OTHER
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Pred. No. 5.8e-30;
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PN JP 2002
PD 15-JAN-
PF 07-AUG-
PR 05-AUG-
PI JEAN BA
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    PC C12N5
C12N15/00
CC EST a
FH Key
                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 203)

Edwards, J. B.D. M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Patent: JP 2002010789-A 12587 15-JAN-2002;
                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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EST and encoded human protein
BD120510
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                             GIORDANO
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GCATAATTTGTGGT 134
                                                                                                       Homo sapiens (human)
JP 2002010789-A/12587
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEANN BAPUTIST DUWAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
                                                                               C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
EST and encoded human protein
Location/Qualifiers
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EP 1104808-A 16454 06-JUN-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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RESULT 9
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Sequence
AX985653
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 16456 28-OCT-2003;
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                           Homo sapiens (human)
                                                  AX985653.1 GI:40991793
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/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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73.1%;
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                                                                                    PAT 15-JAN-2004
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RESULT 10
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AUTHORS
TITLE
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KEYWORDS
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Matches 98
Query Match
Best Local Similarity
Matches 98; Conserv
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TITLE
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Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Patent: JP 2002010789-A 12589 15-JAN-2002;

GENSET CORP
                                                                                                                                                                  PC C12N5/10,C12P21/02,C12P21/08,C12Q1/(
C12N15/00
CC EST and encoded human protein
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source /organism='Homo sapi
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Patent: EP 1104808-A 16456 06-JUN-2001;
Genset (FR)
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EST and encoded human protein.

    AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU

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JP 2002010789-A/12589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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98; Conservative
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60.5%; Score 127.6; DB 6; ilarity 73.1%; Pred. No. 5.9e-30; Conservative 32; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
JP 2002010789-A/12589
15-JAN-2002
                                                                                                                                                                                                                                                                                 C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19,
                                                                                                                                                                                                                                                                                                                 JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
                                                                                                                                                                                                                                                                                                                                   07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
                                                                                                                                             /organism='Homo
                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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73.1%; Pred. No. 5.9e-30;
tive 32; Mismatches 4
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                               Length 231;
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FEATURES
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AUTHORS
TITLE
JOURNAL
MEDLINE
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ACCESSION
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AR424955
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Best Local S
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AR424955
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                                            Unclassified.

1 (bases 1 to 355)

1 (bases 1 to 355)

Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.

EST's and encoded human proteins

Patent: US 6639063-A 16452 28-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 301)

Monstein, H.J., Westin, G., Philipson, L. and Pettersson, U.

A candidate gene for human Ul RNA

EMBO J. 1 (1), 133-137 (1982)
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                                                                                                                              Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
83._.246
                                   Location/Qualifiers
organism="unknown"
/mol_type="genomic
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                           . 355
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patent US
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BD120508
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Best Local S
Matches 98
  AUTHORS
TITLE
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Matches
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TITLE
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EST and encoded human pro
BD120508.1 GI:23215418
BD120508.1 GI:23215418
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Sequence
AX985649
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 355) Edwards,J.B.D.M., Jobert,S. and Giordano,J.B. EST and encoded human protein
                                                               Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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73.1%; Pre
ative 32;
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protein.
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Pred. No. 5.9e-30;
2; Mismatches 4
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                                        Hominidae;
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120 120 60 60

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REFERENCE
AUTHORS
TITLE
ORIGIN
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ORGANISM
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KEYWORDS
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HUMSNU1C1
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GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/12585
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N15/00
CC C12N15/00
CC C12N15/00
CC EST and encoded human protein
CC EST and encoded human protein
FT source 1 . 355
FT source /organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GCATAATTTGTGGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 362)

Bernstein,L.B., Manser,T. and Weiner,A.M.

Human U1 small nuclear RNA genes: extensive conservation of flanking sequences suggests cycles of gene amplification and
                                                                                                                                                                                                        86284656
3837185
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M28012.1 GI:338271
U1 small nuclear RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                   Original source text: Human blood DNA, Location/Qualifiers
                                                                                                                                                                                                                                          transposition Mol. Cell. Bio
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Human U1 small nuclear RNA gene,
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                                                                                                       organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                            'gene="RNU1"
                                                        'gene="RNU1"
                                                                           /map="1p36.1"
L08. .271
          'note="Ul small nuclear RNA; G00-119-560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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73.1%; Pred. No. 5.9e-30;
tive 32; Mismatches 4
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clone cosD1,
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                                                         168 ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCAAATGTGGGAAACTCGACT
                       121 GCAGAAUUGGCGAU 134
                                                                                                                    108 ATACTTACCTGGCAGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
228 GCATAATTTGTGGT 241
                                                                                    61 аиссаниесасиссеваненесивасскиесваниисскогаланеневалального
                                                                                                                                       1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCCAGGGCGAGGCUU
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Search completed: January 19, 2005, 17:47:31 Job time : 1518 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2002as:*
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Gapop 10.0 , Gapext 1.0
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211
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SUMMARIES
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121.2	121.2	122	126		127.6		127.6					127.6	127.6	127.6	127.6	127.6	127.6	127.6	143.8	205.4	Score
57.4	57.4	57.8	59.7	59.7	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	68.2	97.3	Query Match
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ACH71233	ACH84933	AAT96717	AAX84883	AAT39399	ADI37256	ADF13110	AAH14832	ADL31195	AAK94440	AAS64548	ADL31299	AAK94493	AAH07536	ADL29877	ADL28611	AAK93450	AAK92184	ABA92582	ADI34065	AAV32602	ID
Ach71233 Human gen	Ach84933 Human gen	Aat96717 Human REN	Aax84883 Human Ul	Aat39399 U1 RNA. 3	Adi37256 Hypermeth	Adf13110 Hypermeth	Aah14832 Human cDN	Adl31195 Full leng	Aak94440 Human cDN	Aas64548 DNA encod	Adl31299 Full leng	Aak94493 Human ful		Adl29877 5' end of	Adl28611 5' end of	Aak93450 Human cDN	Aak92184 Human cDN	Aba92582 U1DNA amp	Adi34065 N-SMase h	Aav32602 Chimeric	Description

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	
102.6	103	104.8	106.2	106.8	108	109	109.6	110	111.6	112.2	115.6	115.6	115.6	115.6	115.6	115.6	115.6	115.8	115.8	116.4	116.8	119.4	
48.6	48.8	49.7	50.3	50.6	51.2	51.7	51.9	52.1	52.9	53.2	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.9	54.9	55.2	55.4	56.6	
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ADF13089	AAC14652	AAI88559	ADD27762	ADD27764	ADD27761	ADD27763	ACH68354	AAA87354	AAC32349	AAD39652	AAK80091	AAK80096	AAK80092	AAK80097	AAK80093	AAK80094	AAK80095	AAS64549	AAS69273	ADD27746	AAQ89146	AAI95431	
Adf13089 Hypermeth	Aac14652 Human sec	Aai88559 Human pol	Add27762 pGem3z+:U	Add27764 pGem3z+:U	Add27761 pGem3z+:U	Add27763 pGem3z+:U	Ach68354 Human gen	Aaa87354 Rat hepat		Aad39652 Human sma	Aak80091 Human imm	Aak80096 Human imm	Aak80092 Human imm	Aak80097 Human imm	Aak80093 Human imm	Aak80094 Human imm	Aak80095 Human imm	DNA en	Aas69273 DNA encod	6	Aaq89146 RNA moiet	Aai95431 Human neu	

ALIGNMENTS

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	/function= "Cararytic domain" 167181		163	/"Cag= n /note= "Hammerhead ribozyme loop"	-	t mRNA molecule	н			=	/*tag= f	2	/*tag= e	94119	/*tag= d	5093	/*tag= c	9	=	₃g= b	7	=	/*tag= a		Location/Qualifiers						e; huntingdon's disease; heredita	Ul snRNA gene; hammerhead ribozyme loop; growth factor;	•	JA.	(titol cilci)					rd: RNA: 212 BP.		

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a chimeric UI snRNA molecule which CC comprises of a 5' and 3' end unmodified stem loop structure separated by CC the antisense core sequence. The antisense core sequence would itself CC comprise of the first 15 coding nucleotides of the fibrillin mRNA CC followed by the 22 bp hammerhead ribozyme loop which is followed by CC coding nucleotides 17-30 of the fibrillin mRNA. The whole chimeric snRNA CC molecule is an example of a novel nucleic acid construct for suppressing CC expression of a target gene. In the example given, the target gene was CC the fibrillin gene. The antisense core sequence of the chimeric snRNA CC molecule would basepair with the fibrillin mRNA, thus suppressing its CC translation. The invention claims that such nucleic acid constructs can be used for suppressing claimed to be useful for producing non-human CC molecule would save also claimed to be useful for producing non-human CC alzheimer's disease, Huntingdon's disease, hereditary Parkinsonism and CC translatic disease, Huntingdon's disease, hereditary Parkinsonism and CC alzheimer's disease, Therefore, the construct may be useful for treating CC Alzheimer's disease, Therefore, the construct may be reful for treating construct inherited disease, They may also be useful for treating enzymatic CC related disorders, and for reducing expression of growth factors, toxic CC peptides, ligands, receptors or other proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 206
                ADI34065
                                                    ADI34065 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                  125 AAUUGGCGAUCUCCAGCACUGAUGAGUCCGUGAGGACGAAACGCCCUCGACGCAUCUAGU
                                                                                                                                                                                                                                                                                                                                                                                                                                   206;
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                                                                                                                                                                                                                                                                                  AUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCCAAAUGUGGGAAACUCGACUGCAG
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/note= "Forms double stranded region with bases 1-15
the target mRNA molecule (AAV32603)"
187. .212
/*tag= k
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                                                    RNA;
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99.5%;
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                                                                                                                                                                                                                                                                        Matches 172;
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                                                                                                                                                                                                                                                                          Sequence 208 BP; 48 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 1; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule comprising a ribozyme that is specific for N-SMase mRNA, useful for treating inflammatory disorders such as arthritis, osteoarthritis, Crohn's disease, obesity, diabetes, HIV, or liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; ribozyme; N-SMase mRNA; neutral sphingomyelinase inhibition; apoptosis; atherosclerosis; inflammatory disorder; arthritis; crohn's disease; obesity; diabetes; HIV; liver disorder; cirrhosis; excessive cholesterol; renal failure; central nervous system; CNS disorder; depression; schizophrenia; Alzheimer's disease; hammerhead
                                                                                                                                                                                                                                                                                                              hammerhead ribozyme.
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23-OCT-2002; 2002US-00279215.
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                                                                                                                                                                                                                                                                                                                             Alzheimer's disease. The present sequence represents the
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                                                        GGCCACCGGAUGUGCUGACCCCUGCGAUUUUCCCCCAAAUGUGGGAAACUCGACUGCAGAAU
                                                                                        GCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAAUGUGGGAAAACUCGACUGCAGAAU
                                                                                                                             CUUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUUAUCCAUU
                                                                                                                                                    CCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUCCCAGGGCGAGGCUUAUCCAUU
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186. .207
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151. .162
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Pred. No. 4.7e-40;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying anti-extractable nuclear antigen (ENA) antibody based on reaction of antigen complex with specimen, applicable in diagnosis collagen diseases e.g. systemic erythematodes and skin toughening.
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11-JAN-2000;
02-MAY-2000;
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su A, Sugiyama T, Nagai K, Kojima
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                           GCAGAAUUGGCGAU 134
                                                         ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCCAAATGTGGGGAAACTCGACT
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2000JP-00183765.
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                                                                                                                                                                                          60.5%; Score 127.6; DB 4 73.1%; Pred. No. 3.6e-34;
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               20-MAY-2004
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11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                            ADL28611;
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na T, Nagai
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K, Kojima
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Matches
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Best Local
                                               oligo-capping method;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is the 5' end of a full length human cDNA sequence of the invention.
  Homo sapiens
                                                                          human; medicine; signal transduction;
                                                                                                                                                                                  20-MAY-2004
                                                                                                                                                                                                                                    ADL29877;
                                                                                                                                                                                                                                                                                    ADL29877 standard; cDNA; 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-00194486
11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183865
07-JUL-2000; 2000EP-00114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 644; 1340pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REAS-)
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                                                                                                                            of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCCAGGGCGAGGCUU |:||::|||::|||||||||||::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUCCAUUGCACUCCGGAUGUGCCGACCCCUGCGAUUUCCCCAAAUGUGGGAAACUCGACU
                                                                                                                                                                                                                                                                                                                                                                                                              GCATAATTTGTGGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCAAATGTGGGAAACTCGACT
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                                                                                                                            representative human cDNA cluster SeqID 1910
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                                                                                                                                                                            (first entry)
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73.1%; Pr
tive 32;
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na T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127.6; | Pred. No. 3.6e
                                                                       glycoprotein; transcription;
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RESULT 8
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Best Local Similarity
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polymucleotide sequence is the 5' end of a representative human DNA cluster of the invention.
                            28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:4371.
                                                                                                                                                                                                                                                                                                                         26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                          AAH07536;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAH07536 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000;
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                                                                                                                        EP1074617-A2
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 18; SEQ ID NO 1910; 1340pp; English
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gth human cDNAs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RES ASSOC BIOTECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 99JP-00194486.
; 2000JP-00118774.
; 2000JP-00183865.
; 2000EP-00114089.
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                                                                                                                                                                                                                        detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                                                       entry.
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ma T, Nagai K, Kojima
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                                                                                                                                                                                                                                                                                                                                                                                                                           781
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                                                                                                                                                                                                                        antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-34;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 end sequence complementary to a polynucleotide comprises a 3 end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5 end sequence/3 end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH30316 to AAH13628 and confidence and the abnormality of the proteins encoded by the AAH333 to AAH3942 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH3629 to AAH3632 represent or present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300233.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 781 BP; 168 A; 248 C; 207 G; 148 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                     06-NOV-2001
                                                                                                                                             AAK94493 standard; cDNA; 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (a) an oligo-dT primer and an oligonucleotide complementary to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                       GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                                                                               AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUUCCCCCAAAUGUGGGAAACUCGACU
                                                                                                                                                                                                                                                                                                                                                                                                                   AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4371; 2537pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T,
T, Wakamats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.5%; Score 127.6; 73.1%; Pred. No. 3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 781;
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Human;

full length cDNA; cDNA synthesis; oligo-capping;

Human full-length cDNA, SEQ ID NO: 3332

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RESULT 10
ADL31299
ID ADL31
XX
AC ADL31
XX
DT 20-MA
XX
Full
DX
KW human
KW oligo
XX
OS Homo
XX
XX
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                       human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
                                                                                  Full length human cDNA clone SeqID 3332.
                                                                                                                                                                      ADL31299 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                Homo sapiens
                                                                                                                20-MAY-2004
                                                                                                                                             ADL31299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 Primers useful for synthesizing full length cDNA clones and their in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID NO 3332; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                      GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                               GCATAATTTGTGGT
                                                                                                                                                                                                                                                                                                                                                       ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                              (first entry)
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                                                                                                                                                                      cDNA; 1858
                                                                                                                                                                                                                                                                                                                                                                                                              60.5%; Score 127.6; DB 4
73.1%; Pred. No. 5.1e-34;
tive 32; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
na T, Nagai
                                                                                                                                                                                                                                            134
                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                               4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1858;
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T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 11
AAS64548/c
ID AAS645.
XX AAS645.
XC ACCANOMINATION ACCANOMINATION
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
  30-MAR-2001; 2001WO-US008631.
                                                                                                         WO200175067-A2
                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #352
                                                                                                                                                                                                                                                                                                                                                                                              AAS64548
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS64548 standard; cDNA; 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 3332; 1340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligonuclectide primers (830 cDNAs) useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ADL31300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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; 2000JP-00118774.
; 2000JP-00183865.
; 2000EP-00114089.
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a T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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i K, Kojima
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S, Otsuki
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                                                                                                                                                                                                            disorder;
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T, Ko
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RESULT 12
AAK94440
ID AAK94
XX AAK94
AC AAK94
XX O7-NC
DT O7-NC
XX Humar
XX Human
XX Human
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc sequences. (I) is useful as hybridisation probes, polymerase chain cc reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cc and in recombinant production of (II). The polymuclocitides are also used cc in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is conjugate to the sequence against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food conjugate till and the sequence useful in medical imaging conjugate to the sequence of the sequences of the sequences in the sequence of the sequences of data and polymuclocities sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or their traits to assess biodiversity cresponsible for genetic disorders or their traits to assess biodiversity conditions and sequences of the invention. Note: The sequence data for this cc gatent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 352; 103pp; English.
                   Homo sapiens
                                                   Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                    07-NOV-2001
                                                                                                                                                      AAK94440;
                                                                                                                                                                                       AAK94440 standard; cDNA; 1914 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1912 BP; 520 A; 521 C; 547 G; 321 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
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23-AUG-2000; 2000US-00649167.
                                                                                 Human cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                           GCATAATTTGTGGT 13
                                                                                                                                                                                                                                                                                                          GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                   SEQ ID NO: 3228.
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.5%; Score 127.6;
73.1%; Pred. No. 5.20
tive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ADL31195
ID ADL2
XX
AC ADL3
AC ADL3
DT 20-N
XX
DT 00-N
XX
DT 00-N
XX
DT 00-N
XX
DT 00-N
XX
DT 0110
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a human cDNA provided in the specification. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999; 99JP-00194486
11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                           human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1914 BP; 554 A; 501 C; 400 G;
                                                             Homo sapiens
                                                                                                                                          Full length human cDNA clone SeqID 3228
                                                                                                                                                                           20-MAY-2004
                                                                                                                                                                                                           ADL31195
                                                                                                                                                                                                                                           ADL31195 standard; cDNA; 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 3228; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          830 Primers useful for synthesizing full length cDNA clones in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000EP-00114089
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                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                     61 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCCAAAUGUGGGAAACUCGACU 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 АИАСПИАССИВСЕЛЕВАВАНАССАИВАИСАСВАЛЕВИИЛИСССАВОВСЕЛЕНИИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.5%; Score 127.6; DB 4 73.1%; Pred. No. 5.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Hayashi K,
na T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 1914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hii S, Kawai Y;
Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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10-MAR-2004

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RESULT 14
AAH14832
ID AAH14
XX AAH14
XX AAH14
XX DE Human
XX Human
XX Homo
XX Homo
XX Homo
XX O7-FE
XX O7-FE
XX PF 28-JI
PR 27-AI
PR 27-AI
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Best Local S
Matches 98
29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
                                              28-JUL-2000;
                                                                     07-FEB-2001
                                                                                          EP1074617-A2
                                                                                                                                        Human; primer;
                                                                                                                                                             Human cDNA sequence SEQ ID NO:12648.
                                                                                                                                                                                       26-JUN-2001
                                                                                                                                                                                                              AAH14832;
                                                                                                                                                                                                                                  AAH14832 standard; cDNA; 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1914 BP; 554 A; 501 C; 400 G; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotide primers length human cDNAs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                               GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                                                                                           GCATAATTTGTGGT 136
                                                                                                                                                                                                                                                                                                                                      ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCAAATGTGGGAAACTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                   ATACTTACCTGGCAGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                               AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3228; 1340pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00194486.
2000JP-00118774.
2000JP-00183865.
2000EP-00114089.
                                            2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2000JP-00118776
                                                                                                                                                                                      (first
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                      99JP-00248036.
            99JP-00300253
                                                                                                                                       detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                              60.5%;
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la T, Nagai
                                                                                                                                    diagnosis; antisense therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127.6; DB 12;
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                                                                                                                                                                                                                                   ВP
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K, Kojima
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S, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other;
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T, Koga
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                                                                                                                                    therapy;
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                                                                                                                                     88
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ADF13110
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XX ADF13
XX ADF13
XX I2-FE
XX I2-FE
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XX DNA II
KW D
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Matches 98
DNA methylation; CpG dinucleotide rich region; differential methylation hybridisation; DMH; CpG island; screening breast cancer; prostate cancer; colon cancer; lung cancer; liver ca ovarian cancer; human; HBC; hypermethylation in breast cancer; ds.
                                                                                                                                                                                                                          Hypermethylation site in human breast cancer CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13672 represent human amino acid sequences; and AAH13632 to AAH33632 represent human amino acid sequences; and AAH13632 to AAH36883
                                                                                                                                                                                                                                                                                                                                                                                                       ADF13110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 / length cDNAs defined in the specification. Where a primer set computent of the complementary to the complemen
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09-JUN-2000; 2000JP-00241899.
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Sugiyama T, Wakamats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 118067
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A, Nagai K,
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Search completed: January 19, 2005, 17:22:12 Job time: 288 secs
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of detecting DNA methylation of CC a CpG dinucleotide rich region of a nucleic acid. The method comprises CC hybridisation by differential methylation hybridisation (DMH) in which CC the nucleic acid is digested into fragments in which CpG islands are CC linker primer products to digest unmethylated CpG sequences, amplifying CC and labelling the remaining linker primer products and detecting labelled CC fragments fixed to a solid support where each fragment is a CpG CC dinucleotide rich fragment comprising at least 200 nucleotides of which CC at least 50% are guanine and cytosine. Nucleic acid probes prepared from CC acil sample are used to screen CpG dinucleotide rich fragment comprising at least 200 nucleotides of conto a screening array. The invention is useful to diagnose and monitor CC prognosis of a disease associated with aberrant DNA methylation, CC especially breast, prostate, colon, lung, liver or ovarian cancer, CC especially breast prostate, colon, lung, liver or ovarian cancer, CC hypermethylation in human breast cancer at a CpG island locus (HBC, hypermethylation in breast cancer).
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Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Differential methylation hybridization assay for detecting hypermethylation of CpG dinucleotide rich regions in genomic DNA is useful to diagnose and monitor breast, prostate, colon, lung, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; SEQ ID NO 32; 32pp; English.
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18-FEB-1999; 99US-0120592P.
04-FEB-2000; 2000US-00497855.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-621-976-16456
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ALIGNMENTS	US-09-919-172-99 US-09-976-594-811 US-08-862-337-2 US-08-862-337-2 US-08-324-362-4 US-08-324-362-4 US-08-324-362-5 US-09-276-533A-4 US-09-276-533A-4 US-10-158-735-4 US-10-158-735-4 US-10-158-735-4 US-10-158-735-4 US-10-158-735-6 US-09-918-666-18 US-09-918-666-18 US-09-918-666-1 US-08-464-073-26 US-08-464-073-26 US-08-489-039A-1569 US-08-489-039A-1569	
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CILL STATE: C., STATE: C., COUNTRY: USA COUNTRY: USA ZIP: 92037 ZIP: 92037 COMPUTER READABLE FORM: MEDITOR TYPE: Diskettee COMPUTER: DISK Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FRSESEQ for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/724,354D FILING DATE: 01-OCT-1996 PRIOR APPLICATION NUMBER: 60/016,482 FILING DATE: 29-APR-1996 ATTORNEY/AGENT INFORMATION: NAME: Halle, Lisa A. REGISTRATION NUMBER: 07265/09 TELECOMUNICATION INFORMATION: TELEPHONE: 619-678-5070 TELEFAX: 619-678-5079 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 215 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: linear TOY: linear TOY: linear US-08-724-354D-26 RESULT 1 Sequence 26, Application Patent No. 5994119 GENERAL INFORMATION: APPLICANT: Dietz, F TITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: ADDRESSEE: 26, Application 5. 5994119 E: Fish & Richardson, 4225 Excutive Square, Harry C. Harry C. HARRY C. HARRY C. HARRY C. HARRY C. 29 US/08724354D P.C. Suite

Query Match
Best Local Similarity
Matches 194; Conserv

194;

Conservative

76.2%; 90.7%;

Score 160.8; DB Pred. No. 4e-49; 0; Mismatches 1

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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        TOPOLOGY: 11 MOLECULE TYPE:
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 4225 Excutive Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dietz, Harry C. TITLE OF INVENTION: MAMMAL TITLE OF INVENTION: NONSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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SOFTWARE: FastSEC
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                                                                 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCCAAAUGUGGGAAACUCGACU
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ilarity 90.7%;
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                                                                                                                                    Best Loc
Matches
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEO ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16456
LENGTH: 231
TYPE: DNA
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FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16454
LENGTH: 203
TYPE: DNA
USAN 1020-1615
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GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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1 ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
                                                                                                                                  h 60.5%; Score 127.6; DB 4; Similarity 73.1%; Pred. No. 5.7e-37; 98; Conservative 32; Mismatches 4;
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ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
                                                                                                    AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
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GCAGAAUUGGCGAU 134

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APPLICANT: HUANG, HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
CURRENT FILING LATE: UMO1523
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 32
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SEQ ID NO 16452
LENGTH: 355
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Patent No. 6639063
                                                                                                                Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTs and Encode
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens;
                                                                                                                                                                                                                                                         LENGTH: 118067
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Local Similarity 73.1%;
59420 ATACTTACCTGGCAGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT 59479
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                        AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUCCCAGGGCGAGGCUU 60
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                                                                                                                60.5%;
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                                                                                        ; Score 127.6; DB 4; Length 118067; ; Pred. No. 9.7e-36; 32; Mismatches 4; Indels 0;
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Pred. No. 6.9e-37;
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-621-976-16457
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Sequence 16457, Application US/09621976
PATENT NO. 6639063
GENERAL INFORMATION:
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US-09-621-976-16458
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                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16457
LENGTH: 189
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SEQ ID NO 16458
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Best Local (
                                                                   Matches
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Best Local Similarity
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TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                       TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: GENSET.054P2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21
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1 ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
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                                                                   97; Conservative
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                                                                                     Similarity
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72.4%; Pred. No. 7.5e-37;
1tive 33; Mismatches 4
                                                                                   59.7%; Score 126; DB 4; 72.4%; Pred. No. 2e-36;
                                                                 32; Mismatches
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                                                                                                 Length 189;
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GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 16453

LENGTH: 175

TYPE: DNA

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US-09-621-976-16453
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US-09-621-976-16455
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                                                       Matches
                                                                    Query Match
Best Local
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Best Local :
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APPLICANT: Giordano, J.Y.
IITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000.07-21
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                                                                                                                               ORGANISM: Homo sapiens
                                                                    Local Similarity
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1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU |:||::|||:||||||||||||::|
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                                                     Conservative
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                                                               58.4%; Score 123.2; DB 74.2%; Pred. No. 2e-35;
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                                                  Mismatches
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                                                                              DB 4;
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; MOLECULE TYPE:
US-08-704-170-75
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APPLICATION UNBER: US 08/029
FILING DATE: 11-MAR-193
ATTORNEY/AGENT INFORMATION:
NAME: SPICALS, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920
TELECOMMUNICATION INFORMATION:
TELEPAN: (213) 977-1001
TELEPAN: (213) 977-1003
INFORMATION FOR SEQ. ID NO: 75:
                                                                                                                                                                                          Matches 121; Conservative
                                                                                                                                                                                                       Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
STATE: California
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                                                                              AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCCAAAUGUGGGGAAAACUCGACU
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GCAUAAUU
                                                               AGCCAUUGCACUCCGGUUGUGCUGACCCCUGCGAUUUUCCCCAAAUGCGGGAAACUCGACU
                                                                                                                            AUACUUACCUGGCAGGGGAGAUACCAUGAUCAUGAAGGUGGUUCUCCCAGGGCGAGGCUC
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201 No. 5707626th Figueroa Street, Suite
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Takehana, Yoshi
Ehresmann, Glenn
                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                       55.4%;
94.5%;
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                                                                                                                                                                                        Score 116.8; DB 1
Pred. No. 4.3e-33;
0; Mismatches 7
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                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                           Indels
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RESULT 13
US-09-513-999C-36424/c
J. Sequence 36424, Application US/09513999C
J. Patent NO. 6783961
J. GENERAL INFORMATION:
GENERAL INFO
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PCT-US94-02631-75
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/ MOLECULE TYPE:

PCT-US94-02631-75
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Best Local Similarity
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTIN: Expressed Sequence Tags and Encoded Human Proteins.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIA Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US94/02631
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Takehana, Yoshi
APPLICANT: Ehremann, Glenn
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 977-1003
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201 North Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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94.5%; Pred. No. 4.36
tive 0; Mismatches
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                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10271
LENGTH: 157
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 36424
LENGTH: 365
                                                                                                         Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10271, Application US/09621976 Patent No. 6639063
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Best Local Similarity
                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054P2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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LOCATION: 241
OTHER_INFORMATION: w=a
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NAME/KEY: misc_feature
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OTHER INFORMATION: n=a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 GGCGAU 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 CACTCCGGATGTGCCGACCCCTGCGACTCCCCCAAATGTGGGAAACTCGACTGCATAATT 8
 61 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAAUGUGGGAAACUCGACUGCAGAAUU 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUUAUCCAUUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                         Similarity
                                      AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGGT 2
                                                                                                           Conservative
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                                                                                                       48.9%; Score 103.2; DB 74.0%; Pred. No. 4e-28; ative 27; Mismatches
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73.8%; Pred. No. 4.9e-31;
ative 24; Mismatches 9
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
ITITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
PILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SEQ ID NO 1977
LENGTH: 107
TYPE: DNA
CREATION TO SERVICE TO SERVICE TAGES TO SERVICE TO 
Search completed: January 19, 2005, 18:19:45
Job time : 92 secs
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; NAME/KEY: misc feature
; LOCATION: 97 -
; OTHER INFORMATION: w=a or t
US-09-513-999C-18727
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US-09-513-999C-18727
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Best Local S
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 20
OTHER INFORMATION: r=a or g
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NAME/KEY: misc_feature
LOCATION: 80
OTHER INFORMATION: w=a or t
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LOCATION: 90
OTHER_INFORMATION: w=a or t
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LOCATION: 39 __
OTHER_INFORMATION: h=a or c or t
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                                                                                                                                              ch 48.8%; Score 103; DB 4; Length 107; I Similarity 72.9%; Pred. No. 3.9e-28; 78; Conservative 28; Mismatches 1; Indels
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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/Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-10-775-169-82	IIS-10-027-632-32256	115-10-027-632-32256	US-10-029-386-4428	US-10-029-386-18128	US-10-081-327-32	US-10-027-632-286819	US-10-027-632-286819	US-10-276-302-3	US-10-446-519-2	US-10-446-519-1	US-09-163-289A-3	ID
Sequence 8	Segmence 3			Sequence 1	Sequence 3	Sequence 2	Sequence 2	Sequence 3	Sequence 2	Sequence 1,	Sequence 3, Appli	Description
82, Appl)	מאפכנו	4428, Ap	18128, A	32, Appl	286819,	286819,	e 3, Appli	, Appli	, Appli	Appli	

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US-10-003-806-10 US-10-108-260A-2355 US-09-974-879-105 US-09-305-736-105	US-10-027-632-272383 US-10-027-632-272384 US-10-027-632-272381 US-10-027-632-272382 US-10-027-632-272383	US-10-085-783A-55655 US-09-918-995-5448 US-10-027-632-272381 US-10-027-632-272382	US-10-752-986-79 US-10-752-986-79 US-09-919-039-216 US-10-133-013-33 US-09-919-172-88 US-10-752-986-88 US-10-752-986-88	US-10-719-993-6890 US-09-804-481-1 US-10-029-386-1549 US-10-027-632-256774 US-10-027-632-256774 US-10-027-632-230834 US-10-027-632-230834 US-10-027-632-230834	US-10-027-632-79716 US-10-027-632-314864 US-10-027-632-79716 US-10-027-632-314864
Sequence 2,2394, Sequence 10, Appl Sequence 2355, Ap Sequence 105, App Sequence 105, App		Sequence 55655, A Sequence 5448, Ap Sequence 272381, Sequence 272382,	79, App 216, App 216, App 33, App 88, App 88, App 55655,	Sequence 6890, Applia Sequence 1, Applia Sequence 1549, Applia Sequence 256774, Sequence 256774, Sequence 11, Applia Sequence 230834, Sequence 230834,	Sequence 79716, A Sequence 314864, Sequence 79716, A Sequence 314864,

ALIGNMENTS

US-09-163-289A-3

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Patent No. US20020165171A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: DIETZ, Harry
TITLE OF INVENTION: DELIVERY CONSTRUCT FOR ANTISENSE NUCLEIC ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 3
                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 211; Conservative 0;
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PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: JHU1400-1
CURRENT APPLICATION NUMBER: US/09/163,289A
CURRENT FILING DATE: 1998-09-29
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 211
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
  61
                           61 AUCCAUUGCACUCCGGAUGUGCUGACCCCCUGCGAUUUCCCCCAAAUGUGGGAAACUCGACU 120
                                                                                                                         1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU 60
AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAAUGUGGGAAACUCGACU 120
                                                                                              AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
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Pred. No. 5.3e-65;
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CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: 10/279,215
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/342,631
PRIOR PILING DATE: 2001-10-23
INTERESTRIPMENT OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 207
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US-10-446-519-1
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                                  GENERAL INFORMATION:
APPLICANT: CHATTERJEE, SUBROTO B.
APPLICANT: CHATTERJEE, SUBROTO B.
TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 58318-CIP (71699)
CURRENT APPLICATION NUMBER: US/10/446,519
CURRENT APPLICATION NUMBER: 10/279,215
PRIOR APPLICATION NUMBER: 10/279,215
PRIOR APPLICATION NUMBER: 10/279,215
PRIOR APPLICATION NUMBER: 60/342,631
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/342,631
PRIOR FILING DATE: 2001-10-23
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APPLICANT: CHATTERJEE, SUBROTO B.
TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 58318-CIP (71699)
SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10446519 Publication No. US20040006039A1
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ORGANISM: Homo sapiens
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87.0%;
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Pred. No. 1.2e-44;
0; Mismatches 25;
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RESULT 5
US-10-027-632-286819/c
US-10-027-632-286819/c
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; Publication No. US20020198371A1
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; ORGANISM: Homo
US-10-446-519-2
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 164
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10276302
Publication No. US20030152967A1
GENERAL INFORMATION:
APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Murakami, Akihiro
APPLICANT: Kojima, Kasuo
TITLE OF INVENTION: Methods and Kits for measuring antibodies against ENA
FILE REFERENCE: P021101
CURRENT APPLICATION NUMBER: US/10/276,302
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: UF P2000-157410
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 139;
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Best Local
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OTHER INFORMATION: Description of Artificial Sequence:Artificially
OTHER INFORMATION: synthesized primer sequence
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                                                                                                                                               GCATAATTTGTGGT 134
                                                                                                                                                                                  GCAGAAUUGGCGAU 134
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                                                                                                                                                                                                                                                                                                      ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGTTTTCCCAGGGCGAGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCATTGGCCTCCGGATGTGCTGACCCCTGCGATTTCCCCCAAATGTGGGAAACTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                  60.5%; Score 127.6; DB 15; 73.1%; Pred. No. 3e-35; tive 32; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
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APPLICANT: Wang, David G.

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Sequence 286819/c

Sequence 286819, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
ITITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/18,066

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,318

PRIOR APPLICATION NUMBER: US 60/185,358

PRIOR APPLICATION NUMBER: US 60/185,358
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-09
PRIOR TILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-09
PRIOR FILING DATE: 1990-09-09
PRIOR FILING DATE: 1990-09-09
PRIOR FILING DATE: 1990-09-09
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NAME/KEY: misc_feature
LOCATION: (1)...(553)
OTHER INFORMATION: n = A,T,C
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73.1%; Pred. No. 3.9e-35;
tive 32; Mismatches 4
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US-10-081-327-32
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                                                                                                                                                                                        Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/10081327
publication No. US20030129602A1
GEMERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
CURRENT APPLICATION NUMBER: US/10/081,327
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION UNMBER: 06/120,592
PRIOR PRICATION UMBER: 06/118,760
PRIOR APPLICATION UMBER: 06/118,760
PRIOR APPLICATION UMBER: 06/118,760
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 286819
LENGTH: 553
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(553)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens;
                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                   LENGTH: 118067
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                                                          59480 ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCAAATGTGGGAAACTCGACT
59540 GCATAATTTGTGGT 59553
                                                                                                                           59420 ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
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                             GCAGAAUUGGCGAU 134
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                                                                                                                                                                                       60.5%; Score 127.6; DB 1
73.1%; Pred. No. 1.3e-34;
tive 32; Mismatches 4
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US-10-029-386-18128

Sequence 18128, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4428
LENGTH: 515
TYPE: NY 515
                             OTHER INFORMATION: MAP TO CHR6.1
OTHER INFORMATION: EXPRESSED IN PE-
OTHER INFORMATION: EXPRESSED IN EU-
OTHER INFORMATION: EXPRESSED IN LU-
OTHER INFORMATION: EXPRESSED IN HE-
OTHER INFORMATION: EXPRESSED IN HE-
OTHER INFORMATION: EXPRESSED IN BO-
OTHER INFORMATION: NT HIT: J00319.
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HOLD SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA_X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18128
LENGTH: 167
TYPE: DNA
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Best Local (
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXTENDED IN EVALUE 3.00e-89

OTHER INFORMATION: EST_HUMAN HIT: AU138351.1, EVALUE 1.00e-70

OTHER INFORMATION: EST_HUMAN HIT: AU138351.1, EVALUE 1.00e-70
                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                   TYPE: DNA
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

N: EXPRESSED IN LUNG, SIGNAL = 3.2

N: EXPRESSED IN HEART, SIGNAL = 3.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

N: NT HIT: JO0319.1, EVALUE 2.00e-96

N: EST_HUMAN HIT: AU138351.1, EVALUE 4.00e-7
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US-10-027-632-32256/c; Sequence 32256, App; Publication No. US2
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-32256
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LENGTH: 798
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Best Local
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Best Local :
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SOFTWARE: FastSEQ for Windows
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                          Local Similarity
                                    121 GCAGAAUUGGCGAU 134
                                                                                146
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GCATAATTTGTGGT 73
                                                                         ATCCATCGCACTCCGGATATGCTGACCCCTGCGATTTTCCCAAATGTGGGAAACTCGACT
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70.9%; Pred. No. 8.26
ative 31; Mismatches
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Application US/10027632 US20030204075A9

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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-19-28
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                           US-10-775-169-82
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APPLICANT: Wyeth
APPLICANT: Burczynsl
APPLICANT: Twine, Ni
APPLICANT: Dorner, N
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SEQ ID NO 82
LENGTH: 127917
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SEQ ID NO 32256
LENGTH: 798
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Publication No. US20040175743A1
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local Similarity
                                         Matches
                                                                                Query Match
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CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
                                                                                                                                                                                                                                                                                                                       APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
APPLICANT: Method for Monitoring Drug Activities In Vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-08-09
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                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GCAGAAUUGGCGAU 134
                                         95;
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                                       57.4%; ilarity 70.9%; Conservative 3:
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                                       31;
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                                Score 121.2; DB 1/,
Pred. No. 2.5e-32;
                                                                            DB 17;
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US-10-027-632-314864/c
; Sequence 314864, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
APPLICAMT: Wang, David G.
TITLE OF INVENTION: Identification and Mappi
TITLE OF INVENTION: Polymorphisms in the Hu
FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79716
LENGTH: 539
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Best Local (
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Publication No. US20020198371A1
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-07-12
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 ATACTTAGCTGGCAGAGGAAATACCATGATCACAAAGGTGGTTTTCCCAGGGTGAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                            61 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUUCCCCAAAUGUGGGGAAACUCGACU 120
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                                                                  and Mapping of Single Nucleotide in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12

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; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-79716
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR FILING DATE: 1999-11-23
PRIOR PPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRStSEQ for Windows Version 4.0
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LENGTH: 539
TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79716
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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Search completed: January 19, 2005, 23:36:58 Job time : 304 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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BP45568 BP455568
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CL118164	CL140772	CL146765	CL090810	CL139212	CL138662	CL145767	CL139756	CL129703	CL130843	CL133632	AW106204	CA841195	CA842042	BB239622	CR007005	CB131782	CR226195	AZ901371	AW318834	CCORCTIG
ISB1-70C1	ISB1-117N	ISB1-147K	ISB1-19B2	ISB1-112B	ISB1-111F	ISB1-146E	ISB1-1120	ISB1-97B2	ISB1-98M7	ISB1-103M	um24e11.y	ip30h03.y	1p27e05.y	BB239622	Forward s	K-EST0181	Forward s	RPCI-24-1	un08b12.y	CLOSETIG

ALIGNMENTS

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Qy Db 2	Query Match Best Local Matches 9	LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT FEATURES BOUICE ORIGIN	RESULT 1
1 AUACUUACCUGGCAGGGAGAUACCAUGAUCACGAAGGUUGUUUUUCCCAGGGCGAGGCUU 60	Query Match 60.5%; Score 127.6; DB 9; Length 362; Best Local Similarity 73.1%; Pred. No. 1.4e-29; Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;	CB310367 tigr-gss-dog-17000360578182 Dog Library Canis familiaris genomic survey sequence. CB310367 CB310367.1 GI:36108130 GSS. Canis familiaris (dog) Canis familiaris (dog) Canis familiaris CBMARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 362) Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Wenter, J.C. The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003) 22875432 1451267 Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0208 Email: ekirknes@tigr.org Class: shotgun. Location/Qualifiers 1. 362 /organisme="Canis familiaris" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /clone_lib="Dog Library" /clone_lib="Dog Library" /clone_lib="Dog Library" /clone_lib="Dog Library" /clone_lib="Dog Library" /clone_lib="Canis familiaris were prepared from peripheral blood"	

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RESULT 3
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                              61
     sequence.
BM749651
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                            \tt BM749651 \tt 556\ bp mRNA linear EST 04-K-EST0024911 S11SNU1 Homo sapiens cDNA clone S11SNU1-4-H10
                                                                                                                                                                                                                                                                            CONSOILLIME C. CONSOILLIME CONSOILLIME CONSOILLIME CONSOILLIME CONSOILLIME CONTROL (DKFZp686L2236) is available at the RZPD in This clone (DKFZp686L2236) is available at the RZPD in Please Contact the RZPD: Ressourcenzentrum, Heubnerweg Please Contact the RZPD: Ressourcenzentrum, Heubnerweg Francharlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 bp mRNA linear EST 04-SEP-2003
DKFZp686L2236_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686L2236_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin-Charlottenburg, GERMAN Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                        ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTTTTTCCCAGGGCGAGGCTT
                                                                                                                                                              GCAGAAUUGGCGAU 134
                                                                                                                                                                                            ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCAAATGTGGGAAACTCGACT
                                                                                                                                GCATAATTTGTGGT 356
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
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/dev_stage="adult"
/lab_host="DH10B"
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
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                                                                                                                                                                                                                                                                                                                                         60.5%;
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                                                                                                                                                                                                                                                                                                                      Score 127.6; DB 1;
Pred. No. 1.5e-29;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                    Length 468;
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                            EST 04-MAR-2002
L-4-H10 5', mRNA
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121 GCAGAAUUGGCGAU 134
BP455568 full-length enriched swine cDNA library, scrofa cDNA clone OVRM10152B01 5', mRNA sequence.
BP455568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU 60
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1 (bases 1 to 556)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (20 Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 4 row: H column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Research Center
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                                                                                                                                                                                                                                                                                                                                                       ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCCAAATGTGGGAAACTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                           AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCCAAAUGUGGGAAACUCGACU 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACTTACCTGGCAGGGGGGGTATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=Torgan: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and CDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME185-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli TopolOf* by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab host="Topl0F'"
/clone_lb="S11SNU1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mkNA"
/db_xref="taxon:9606"
/clone="S11SNU1-4-H10"
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/mol_type="mRNA"
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                                                         adult ovary Sus
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     TITLE
                                                         AUTHORS
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1 (bases 1 to 565)

Uenish1,H., Bguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 567)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                           K-EST0171806 L13SNU387 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
                                                                                                                                                                                   CB123444
CB123444.1
                                                                                                                                  Homo sapiens
                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                          mRNA
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Low quality bases were trimmed based on the quality values
    Location/Qualifiers
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EST.
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Frontier Korean EST Project 2001
                                                                                                                                                                                                                          sequence.
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/tissue_type="ovary"
/dev_stage="adult"
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/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                     GI:28082873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%; Score 127.6; DB 5
73.1%; Pred. No. 1.5e-29;
tive 32; Mismatches 4
                                                                                                                                                                                                                                     567 bp ml
                                                                                                                                                                                                                                       mRNA linear EST 29-JAN-2003 s cDNA clone L13SNU387-4-E11 5',
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BP452975
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VERSION
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                                    AUTHORS
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                                                                                                           Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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BP452975 full-length enriched swine cDNA linear EST 30-DEC-2003 scrofa cDNA clone LVRM10159F12 5', mRNA sequence.
BP452975 BP452975.1 GI:40443042
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 602)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H. Okumura,N., Hamasima,N. and Awata,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: yongsung@mail.kribb.re.kr
Plate: 4 row: E column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTTCCCCAAATGTGGGAAACTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized form oilgo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand competed to a DNA strand by Okayama-Berg method. The obbtained cDNA vectors were used for transformation of the cDNA libraries constructed by this method are full-length enriched cDNA library."
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/cell_line="SNU-387"
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/sex="f"
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/db_xref="taxon:9606"
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Shanghai.
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
                                                                                          Unpublished (2000)
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-6474206
Email: mbshi@ms.stn.sh.cn
This Clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                           AV738075
AV738075 CB Homo sapiens
AV738075
AV738075.1 GI:10855656
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                                                                                                                                                                                                                                                    1 (bases 1 to 614)
Zhang, Q., Ye,M., Wu,X., Gu,J., Huang,Q.,
Chen,S., Wao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
Location/Qualifiers
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Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library,
liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LVRM10159F12"
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|mol_type="mRNA"
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e CBUAFG08
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08 5', mRNA sequence.
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RESULT 8
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Query Match
Best Local Similarity
Matches 98; Conserv
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JOURNAL
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                                                                                                                                                                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                       Genomics Laboratory
Helix Research Institute
Kisarazu, Chiba
                                                                                                                                                                                                                                                                                                                                                          1532-3 Yana, Kisarazu, Tel: 81-438-52-3975
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Unpublished (2000)
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AU138351 PLACE1 Homo sapiens
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                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1008378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript; Site_1: EcoRI; cloned randomly with the EcoRI digestion"
                                                                                    /tissue_type="placenta"
/clone_lib="pLACE1"
/note="Vector: pME18SFL
                                                                                                                                                                                                                                Location/Qualifiers
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBUAFG08"
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60.5%; Sc
73.1%; Pr
tive 32;
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Score 127.6;
Pred. No. 1.6e
32; Mismatches
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Pred. No. 1.6e-29;
                                                                                      PME18SFL3"
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cDNA clone PLACE1008378 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                            292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii,S., Saito,K., Kawai,Y.,
ura,Y., Nagai,T., Sugano,S. and
                               DB 1;
                               Length
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RESULT 10
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                                                                                                                                                                                                                                                         98;
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Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 715)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CE201300 715 bp DNA linear GSS 25-SEP-20 tigr-gss-dog-17000372228685 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence CE201300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kirkness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22875432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter, J.C.
                                                                                                                                   ATCCATTGCACTCCGGATGTGCTGACCCCTGCGATTTCCCCCAAATGTGGGAAACTCGACT
                                                                                                                                                 AUCCAUUGCACUCCGGAUGUGCUGACCCCUGCGAUUUCCCCAAAUGUGGGAAACUCGACU
                                                                                                                                                                                            ATACTTACCTGGCAGGGGAGATACCATGATCACGAAGGTGGTTTTCCCAGGGCGAGGCTT
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                                                                                                   GCAGAAUUGGCGAU 134
                                                                                                                                                                                                                          AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
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                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared
peripheral Blood"
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Canis familiaris"
                                                                                                                                                                                                                                                                   60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tion/Qualifiers
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Pred. No. 1.6e-29;
2; Mismatches 4
 742
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 linear
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 EST 30-DEC-2003
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BP437373
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     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 742)

Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H. Okumura, N., Hamasima, N. and Awata, T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
                                                                                                                                                                        BP437373 full-length enriched swine cDNA library, scrofa cDNA clone LNG010036E06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUUCCCAGGGCGAGGCUU
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
1 (bases 1 to 781)
Uenishi,H., Eguchi,T., Suzuki,K., Saw
                                                                           Sus scrofa (pig)
                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out
EST project with full-length (Japan) by National Institute of
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
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                                                                                                                                       BP437373.1
                                                                                                                                                         BP437373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector sequences were eliminated by RepeatMasker version 2002/07/13
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quality bases were trimmed |
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="ovary"
/dev_stage="adult"
/clone_lib="full-length
ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVRM10127B11"
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                                                                                                                                       GI:40427440
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                                       Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
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Pred. No. 1.6e-29;
   Suzuki, K., Sawazaki, T.,
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   Toki, D., Shinkai, H.,
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adult
                                         Euteleostomi;
Sus.
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Best Local S
Matches 98
                                                                                                                                                                                      AUTHORS
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                                                   Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W., Balrymple,B.P. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other_GSSs: CH240_325G6.T7
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                       CC491649 796 bp DNA CH240_325G6.TARBAC13P2 CHORI-240 Bos taurus CH240_325G6, genomic survey sequence.
CC491649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                   CC491649.1
GSS.
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EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                              Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector sequences were eliminated by RepeatMasker version 2002/07/13
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/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="LNG010036E06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      GI:31802563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 127.6; DB 5;
; Pred. No. 1.6e-29;
32; Mismatches 4;
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Best Local S
Matches 98
                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                       scrofa cDNA clone OVR0100
BP144031
BP144031.1 GI:40393502
EST
Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
                                                                                                                                                                                                                                   Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; (Dases 1 to 809)
                                                                                                                                                                                                                                                                                                                                                                                                     BP144031
BP144031 full-length enriched swine cDNA library,
BP163 cDNA clone OVR010018G03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
                                     2 Ikenodai, Tsukuba, Ibaraki 305-8602,
Tel: +81-29-838-8627
                                                                                Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
                       Fax: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 604-877-6276
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huenishi@affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_325G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/mol_type="genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%; Fred
73.1%; Pred
32;
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Pred. No. 1.6e-29;
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                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                   HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU122692
AU122692 MAMMA1 Homo
                                                                                                                                                                                                                                                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                      Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU122692.1
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                                                                                                                                                                                                                                  Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector sequences were eliminated by RepeatMasker version 2002/07/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATAATTTGTGGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGAAUUGGCGAU 134
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quality bases were trimmed based on the quality values
Location/Qualifiers
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                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAMMA1002910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="full-length ovary"
                                                                                               1. .883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVR010018G03"
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                                                      organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="ovary"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Sus scrofa"
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Pred. No. 1.6e-29;
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) 5', mRNA
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RESULT 14 AU122692

DEFINITION

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Matches

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

JOURNAL COMMENT

TITLE

REFERENCE

AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., T
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP433109 full-length enriched swine cDNA library, scrofa cDNA clone LNG010009A02 5', mRNA sequence.
BP433109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 893)
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    AUACTURACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUGGUUUUCCCAGGGCGAGGCUU

                                                                                                                                                                                                                                                                                                                                                                                      Low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +81-29-838-8627
Fax: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bus
                                                                                                                                                                                                                                                                                                                                                                                                                             library
Vector sequences were eliminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP433109.1 GI:40423176
                                                                               Similarity
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AUACUUACCUGGCAGGGGAGAUACCAUGAUCACGAAGGUUGUUUUCCCAGGGCGAGGCUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATAATTTGTGGT 134
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                                                          Conservative
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                                                                                                                                                                             /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9923"
/clone="LNG01009A02"
/tissue type="lung"
/dev_stage="adult"
/clone_lib="full-length e
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/note="Vector: pME18SFL3"
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